SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 21, 2004, 07:44:27 ; Search time 395.202 Seconds
                                            (without alignments)
                                            2698.108 Million cell updates/sec

Title: US-08-737-319(1) *translated → searched in DNA databases*
Perfect score: 1341
Sequence: 1 MSMPNIVPPAEVRTEGLSLE..........KGEVDAKSLEDLSDNKVWKM 251

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US08737319/runat_15042004_131640_26696/app_query.fasta_1.8
46
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08737319_@CGN_1_1_586_@runat_15042004_131640_26696 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_29Jan04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002s:*
                 7: geneseqn2003as:*
                 8: geneseqn2003bs:*
                 9: geneseqn2003cs:*
                 10: geneseqn2004s:*

any DNA encoding SEQ 1

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

(handwritten: action)
(handwritten: on PTO-892 (8/17/1998))
(handwritten: earliest is 12/22/95)

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1341	100.0	1100	2	AAT40216 *(handwritten: Appl WO 96/28545)*	Aat40216 Sequence
2	1341	100.0	1165	2	AAT72945 *(handwritten: WO 91/23633)*	Aat72945 Phaffia c
3	819	61.1	846	9	ADB69660	Adb69660 C. neofor
4	695	51.8	1019	9	ADB69299	Adb69299 C. neofor
5	695	51.8	3019	9	ADB68938	Adb68938 C. neofor
6	640.5	47.8	816	7	ABT19254	Abt19254 Aspergill
7	629	46.9	855	6	ABZ32187	Abz32187 Candida a
8	627.5	46.8	816	7	ABT21074	Abt21074 Aspergill
9	623	46.5	8400	6	AAD31029	Aad31029 Operon G
10	623	46.5	14623	6	AAD31039	Aad31039 Plastid t
11	623	46.5	14623	6	AAD31041	Aad31041 Plastid t
12	621	46.3	684	6	AAD31019	Aad31019 Schizosac
13	579.5	43.2	1807	6	ABK84546	Abk84546 Human cDN
14	579.5	43.2	1807	6	ABN97217	Abn97217 Gene #371
15	579.5	43.2	1807	7	ACA89903	Aca89903 Gene diff
16	579.5	43.2	1920	6	ABQ93307	Abq93307 Human cDN
17	578.5	43.1	867	6	ABK96803	Abk96803 S. cerevi
18	578.5	43.1	1058	2	AAT40218	Aat40218 Sequence
19	571.5	42.6	822	2	AAX39886	Aax39886 Gastric c
20	560.5	41.8	1182	7	ABT42305	Abt42305 Toxicity
21	560.5	41.8	1182	9	ADB56191	Adb56191 Toxicity-
22	560.5	41.8	1182	9	ADB53451	Adb53451 Primary r
23	552.5	41.2	2957	7	ABT18066	Abt18066 Aspergill
24	552.5	41.2	2958	7	ABT19880	Abt19880 Aspergill
25	552	41.2	1271	3	AAZ45588	Aaz45588 Nucleotid
26	552	41.2	1271	6	ABS71576	Abs71576 A. palaes
27	547	40.8	1002	3	AAZ45587	Aaz45587 Nucleotid
28	547	40.8	1002	6	ABS71575	Abs71575 A. palaes
29	546.5	40.8	958	7	ABT18660	Abt18660 Aspergill
30	546.5	40.8	958	7	ABT20476	Abt20476 Aspergill
31	541	40.3	1031	3	AAZ45594	Aaz45594 Nucleotid
32	541	40.3	1031	6	ABS71582	Abs71582 O. sativa
33	534.5	39.9	996	3	AAZ45581	Aaz45581 cDNA enco
34	534.5	39.9	996	6	ABS71569	Abs71569 A. thalia
35	532	39.7	990	3	AAC47123	Aac47123 Arabidops
36	530.5	39.6	855	6	ABZ12767	Abz12767 Arabidops
37	530.5	39.6	880	3	AAZ98352	Aaz98352 A. thalia
38	529.5	39.5	988	3	AAZ45591	Aaz45591 Nucleotid
39	529.5	39.5	988	6	ABS71579	Abs71579 L. sativa
40	528.5	39.4	876	6	ABZ12487	Abz12487 Arabidops
41	527	39.3	954	2	AAT95373	Aat95373 Arabidops
42	527	39.3	954	3	AAZ45580	Aaz45580 cDNA enco
43	527	39.3	954	6	ABS71568	Abs71568 A. thalia
44	525	39.1	698	3	AAF14664	Aaf14664 Aspergill
45	520.5	38.8	985	3	AAZ45590	Aaz45590 Nucleotid

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 21, 2004, 07:44:27 ; Search time 3990.9 Seconds
                                            (without alignments)
                                            2725.977 Million cell updates/sec

Title: US-08-737-319-1
Perfect score: 1341
Sequence: 1 MSMPNIVPPAEVRTEGLSLE..........KGEVDAKSLEDLSDNKVWKM 251

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US08737319/runat_15042004_131641_26703/app_query.fasta_1.8
46
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08737319_@CGN_1_1_3077_@runat_15042004_131641_26703 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*

```
11:  gb_sts:*
12:  gb_sy:*
13:  gb_un:*
14:  gb_vi:*
15:  em_ba:*
16:  em_fun:*
17:  em_hum:*
18:  em_in:*
19:  em_mu:*
20:  em_om:*
21:  em_or:*
22:  em_ov:*
23:  em_pat:*
24:  em_ph:*
25:  em_pl:*
26:  em_ro:*
27:  em_sts:*
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	1341	100.0	1084	8	AB019035	*1997 - GenBank*	AB019035 Xanthophy
2	1341	100.0	1099	6	E12045	JP 1996242861	E12045 cDNA encodi
3	1341	100.0	1099	6	BD014674	JP 2001 136992	BD014674 Method of
4	1341	100.0	1165	6	A63895	WO 97/23633 ✓	A63895 Sequence 20
5	1341	100.0	1165	6	AR366158	6329141 (USPN) Seq 20	AR366158 Sequence
6	1167	87.0	3239	8	PRY15811	1999	Y15811 Xanthophyll
7	695	51.8	93593	8	AF263283		AF263283 Filobasid
8	695	51.8	93979	8	AC068564		AC068564 Filobasid
9	637	47.5	1017	8	AF479816		AF479816 Aspergill
10	629	46.9	855	6	AX489174		AX489174 Sequence
11	621	46.3	931	8	SPU21154		U21154 Schizosacch
12	579.5	43.2	687	9	BT006761		BT006761 Homo sapi
13	579.5	43.2	687	12	BT007937		BT007937 Synthetic
14	579.5	43.2	1288	9	BC019227		BC019227 Homo sapi
15	579.5	43.2	1773	9	AF271720		AF271720 Homo sapi
16	579.5	43.2	1807	6	AX411068		AX411068 Sequence

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OM nucleic - nucleic search, using sw model

Run on: April 21, 2004, 07:44:29 ; Search time 511.316 Seconds
                                          (without alignments)
                                          9690.649 Million cell updates/sec

Title: US-08-737-319-4
Perfect score: 1099
Sequence: 1 CCCACGCGTCCGCACATCTC..........ACTACAAAAAAAAAAAAAAA 1099

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                1:   /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                2:   /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                3:   /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                4:   /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                5:   /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                6:   /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                7:   /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                8:   /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                9:   /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	202.6	18.4	846	16	US-10-320-797-2065	Sequence 2065, Ap
2	182.2	16.6	816	15	US-10-128-714-2424	Sequence 2424, Ap
3	179	16.3	816	15	US-10-128-714-7424	Sequence 7424, Ap
4	126.2	11.5	684	10	US-09-918-740-23	Sequence 23, Appl
5	126.2	11.5	684	10	US-09-918-740-54	Sequence 54, Appl
6	126.2	11.5	8400	10	US-09-918-740-64	Sequence 64, Appl
7	126.2	11.5	14623	10	US-09-918-740-74	Sequence 74, Appl
8	126.2	11.5	14623	10	US-09-918-740-76	Sequence 76, Appl
9	125	11.4	1002	9	US-09-323-998D-28	Sequence 28, Appl
10	124.2	11.3	1271	9	US-09-323-998D-29	Sequence 29, Appl
11	121.4	11.0	1031	9	US-09-323-998D-35	Sequence 35, Appl
12	114.8	10.4	985	9	US-09-323-998D-31	Sequence 31, Appl
13	112.8	10.3	1182	12	US-10-152-319A-2007	Sequence 2007, Ap
14	112.8	10.3	1182	16	US-10-388-934-12	Sequence 12, Appl
15	111.6	10.2	1807	9	US-09-880-107-3712	Sequence 3712, Ap
16	111.6	10.2	1920	13	US-10-363-616-20	Sequence 20, Appl
17	111.6	10.2	2059	10	US-09-814-353-20314	Sequence 20314, A
18	111	10.1	876	9	US-09-938-842A-292	Sequence 292, App
19	111	10.1	876	11	US-09-938-842A-292	Sequence 292, App
20	109.8	10.0	954	9	US-09-323-998D-34	Sequence 34, Appl
21	109.4	10.0	855	9	US-09-938-842A-572	Sequence 572, App
22	109.4	10.0	855	11	US-09-938-842A-572	Sequence 572, App
23	109.4	10.0	880	15	US-10-342-224-95	Sequence 95, Appl
24	109.4	10.0	954	9	US-09-323-998D-9	Sequence 9, Appli
25	109.4	10.0	996	9	US-09-323-998D-10	Sequence 10, Appl
26	107.2	9.8	831	13	US-10-424-599-13178	Sequence 13178, A
27	102.6	9.3	3203	9	US-09-925-302-142	Sequence 142, App
28	102.6	9.3	3203	13	US-09-925-302-142	Sequence 142, App
29	101.8	9.3	867	16	US-10-369-493-46169	Sequence 46169, A
30	99.2	9.0	453	10	US-09-918-995-3039	Sequence 3039, Ap
31	98.8	9.0	988	9	US-09-323-998D-32	Sequence 32, Appl
32	89.6	8.2	1019	16	US-10-320-797-1065	Sequence 1065, Ap
33	89.6	8.2	3019	16	US-10-320-797-65	Sequence 65, Appl
34	89.4	8.1	958	15	US-10-128-714-1424	Sequence 1424, Ap
35	89.4	8.1	958	15	US-10-128-714-6424	Sequence 6424, Ap
36	89.4	8.1	2957	15	US-10-128-714-424	Sequence 424, App
37	89.4	8.1	2958	15	US-10-128-714-5424	Sequence 5424, Ap
38	86.4	7.9	1332	16	US-10-120-988-353	Sequence 353, App
39	86.4	7.9	1359	16	US-10-094-749-1226	Sequence 1226, Ap
40	86.4	7.9	1378	15	US-10-103-313-24	Sequence 24, Appl
41	86.4	7.9	1453	15	US-10-103-313-152	Sequence 152, App
42	77.4	7.0	775	16	US-10-369-493-27183	Sequence 27183, A
43	74.6	6.8	827	16	US-10-369-493-36552	Sequence 36552, A
44	73	6.6	1874	9	US-09-323-998D-33	Sequence 33, Appl
45	72.6	6.6	788	13	US-10-425-114-1629	Sequence 1629, Ap

ALIGNMENTS

RESULT 1
US-10-320-797-2065

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 21, 2004, 07:44:27 ; Search time 4118.1 Seconds
                                            (without alignments)
                                            2725.977 Million cell updates/sec

Title: US-08-737-319(2)   in DNA databases
Perfect score: 1398
Sequence: 1 MQLLAEDRTDHMRGASTWAG..........AALNTDKHEDWGTVHHINEA 259

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US08737319/runat_15042004_131641_26703/app_query.fasta_1.8
46
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08737319_@CGN_1_1_3077_@runat_15042004_131641_26703 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*

Any DNA encoding SEQ:2

```
11:   gb_sts:*
12:   gb_sy:*
13:   gb_un:*
14:   gb_vi:*
15:   em_ba:*
16:   em_fun:*
17:   em_hum:*
18:   em_in:*
19:   em_mu:*
20:   em_om:*
21:   em_or:*
22:   em_ov:*
23:   em_pat:*
24:   em_ph:*
25:   em_pl:*
26:   em_ro:*
27:   em_sts:*
28:   em_un:*
29:   em_vi:*
30:   em_htg_hum:*
31:   em_htg_inv:*
32:   em_htg_other:*
33:   em_htg_mus:*
34:   em_htg_pln:*
35:   em_htg_rod:*
36:   em_htg_mam:*
37:   em_htg_vrt:*
38:   em_sy:*
39:   em_htgo_hum:*
40:   em_htgo_mus:*
41:   em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

1 mismatch (handwritten)

Result No.	Score	% Query Match	Length	DB	ID		Description
						GenBank (handwritten)	
1	1398	100.0	1058	8	AB019034 *1997*		AB019034 Haematoco
2	1398	100.0	1074	6	E12046 *JP 1996 242861*		E12046 cDNA encodi
3	1398	100.0	1074	6	BD014675 *JP 2001 136992*		BD014675 Method of
4	1394	99.7	1099	8	AF082326 *- 1998*		AF082326 Haematoco
5	1394	99.7	1109	6	AR428559 *- 6642021 USPN*		AR428559 Sequence
6	1394	99.7	1109	6	BD223743 *JP 2002*		BD223743 Genes of
7	1383	98.9	1135	6	AR003639 *5744341 USPN (12)*		AR003639 Sequence
8	1383	98.9	1135	6	AR428553		AR428553 Sequence
9	1383	98.9	1135	6	BD223737		BD223737 Genes of
10	1368	97.9	1150	8	AF082325 *-1998*		AF082325 Haematoco
11	1368	97.9	1165	6	AR003638		AR003638 Sequence
12	1368	97.9	1165	6	AR428552		AR428552 Sequence
13	1368	97.9	1165	6	BD223736		BD223736 Genes of
14	777.5	55.6	1860	8	AF082869		AF082869 Chlamydom
15	777.5	55.6	1874	6	AR428562		AR428562 Sequence
16	777.5	55.6	1874	6	BD223746		BD223746 Genes of

earliest US 06/1998 (handwritten, right margin)

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 21, 2004, 07:44:27 ; Search time 407.798 Seconds
                                            (without alignments)
                                            2698.108 Million cell updates/sec

Title: US-08-737-319-2
Perfect score: 1398
Sequence: 1 MQLLAEDRTDHMRGASTWAG..........AALNTDKHEDWGTVHHINEA 259

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US08737319/runat_15042004_131640_26696/app_query.fasta_1.8
46
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08737319_@CGN_1_1_586_@runat_15042004_131640_26696 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_29Jan04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002s:*
                 7: geneseqn2003as:*
                 8: geneseqn2003bs:*
                 9: geneseqn2003cs:*
                 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

earliest 06/1998
Cunningham

SUMMARIES

Appl.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1398	100.0	1134	2	AAT40217 *WO 96/28545*	Aat40217 Sequence
2	1394	99.7	1109	3	AAZ45589 *WO 99/63055*	Aaz45589 Nucleotid
3	1394	99.7	1109	6	ABS71577 *USPAP 2002/02631*	Abs71577 H. pluvia *earliest 03/1996*
4	1383	98.9	1135	2	AAT95391 *WO 97/36998*	Aat95391 Haematoco
5	1383	98.9	1135	3	AAZ45583 *WO 99/63055*	Aaz45583 cDNA enco
6	1383	98.9	1135	6	ABS71571	Abs71571 H. pluvia
7	1368	97.9	1165	2	AAT95390	Aat95390 Haematoco
8	1368	97.9	1165	3	AAZ45582	Aaz45582 cDNA enco
9	1368	97.9	1165	6	ABS71570	Abs71570 H. pluvia
10	777.5	55.6	1874	3	AAZ45592	Aaz45592 Nucleotid
11	777.5	55.6	1874	6	ABS71580	Abs71580 C. reinha
12	538	38.5	816	7	ABT19254	Abt19254 Aspergill
13	527	37.7	988	3	AAZ45591	Aaz45591 Nucleotid
14	527	37.7	988	6	ABS71579	Abs71579 L. sativa
15	527	37.7	1031	3	AAZ45594	Aaz45594 Nucleotid
16	527	37.7	1031	6	ABS71582	Abs71582 O. sativa
17	526	37.6	816	7	ABT21074	Abt21074 Aspergill
18	526	37.6	876	6	ABZ12487	Abz12487 Arabidops
19	526	37.6	990	3	AAC47123	Aac47123 Arabidops
20	523	37.4	1020	3	AAA07585	Aaa07585 Marigold
21	522	37.3	684	6	AAD31019	Aad31019 Schizosac
22	522	37.3	996	3	AAZ45581	Aaz45581 cDNA enco
23	522	37.3	996	6	ABS71569	Abs71569 A. thalia
24	522	37.3	8400	6	AAD31029	Aad31029 Operon G
25	522	37.3	14623	6	AAD31039	Aad31039 Plastid t
26	522	37.3	14623	6	AAD31041	Aad31041 Plastid t
27	521	37.3	954	2	AAT95373	Aat95373 Arabidops
28	521	37.3	954	3	AAZ45580	Aaz45580 cDNA enco
29	521	37.3	954	6	ABS71568	Abs71568 A. thalia
30	517	37.0	1002	3	AAZ45587	Aaz45587 Nucleotid
31	517	37.0	1002	6	ABS71575	Abs71575 A. palaes
32	517	37.0	1288	4	AAC62234	Aac62234 DNA encod
33	517	37.0	1288	5	AAH44118	Aah44118 Hevea bra
34	516	36.9	985	3	AAZ45590	Aaz45590 Nucleotid
35	516	36.9	985	6	ABS71578	Abs71578 L. sativa
36	515	36.8	855	6	ABZ12767	Abz12767 Arabidops
37	515	36.8	880	3	AAZ98352	Aaz98352 A. thalia
38	513	36.7	855	6	ABZ32187	Abz32187 Candida a
39	510	36.5	1271	3	AAZ45588	Aaz45588 Nucleotid
40	510	36.5	1271	6	ABS71576	Abs71576 A. palaes
41	505	36.1	1101	3	AAC46636	Aac46636 Zea mays
42	501	35.8	850	4	ABL10211	Abl10211 Drosophil
43	497.5	35.6	822	2	AAX39886	Aax39886 Gastric c
44	496	35.5	867	6	ABK96803	Abk96803 S. cerevi
45	496	35.5	1058	2	AAT40218	Aat40218 Sequence

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2004, 07:44:29 ; Search time 499.684 Seconds
                                           (without alignments)
                                           9690.649 Million cell updates/sec

Title: US-08-737-319-5
Perfect score: 1074
Sequence: 1 ATCGCTACTTGGAACCTGGC..........CTGGAAAAAAAAAAAAAAAA 1074

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	931	86.7	1109	9	US-09-323-998D-30	Sequence 30, Appl
2	925.6	86.2	1135	9	US-09-323-998D-12	Sequence 12, Appl
3	878	81.8	1165	9	US-09-323-998D-11	Sequence 11, Appl
4	236.2	22.0	1874	9	US-09-323-998D-33	Sequence 33, Appl
5	107.2	10.0	1031	9	US-09-323-998D-35	Sequence 35, Appl
6	94	8.8	816	15	US-10-128-714-2424	Sequence 2424, Ap
7	90.8	8.5	591	15	US-10-156-761-1652	Sequence 1652, Ap
8	90.8	8.5	816	15	US-10-128-714-7424	Sequence 7424, Ap
9	90.8	8.5	9025608	15	US-10-156-761-1	Sequence 1, Appli
10	82.8	7.7	831	13	US-10-424-599-13178	Sequence 13178, A
11	82	7.6	876	9	US-09-938-842A-292	Sequence 292, App
12	82	7.6	876	11	US-09-938-842A-292	Sequence 292, App
13	82	7.6	996	9	US-09-323-998D-10	Sequence 10, Appl
14	80.8	7.5	1002	9	US-09-323-998D-28	Sequence 28, Appl
15	80.4	7.5	855	9	US-09-938-842A-572	Sequence 572, App
16	80.4	7.5	855	11	US-09-938-842A-572	Sequence 572, App
17	80.4	7.5	880	15	US-10-342-224-95	Sequence 95, Appl
18	80.4	7.5	954	9	US-09-323-998D-9	Sequence 9, Appli
19	79.4	7.4	985	9	US-09-323-998D-31	Sequence 31, Appl
20	79	7.4	1271	9	US-09-323-998D-29	Sequence 29, Appl
21	78.4	7.3	775	16	US-10-369-493-27183	Sequence 27183, A
22	74.4	6.9	684	10	US-09-918-740-23	Sequence 23, Appl
23	74.4	6.9	684	10	US-09-918-740-54	Sequence 54, Appl
24	74.4	6.9	8400	10	US-09-918-740-64	Sequence 64, Appl
25	74.4	6.9	14623	10	US-09-918-740-74	Sequence 74, Appl
26	74.4	6.9	14623	10	US-09-918-740-76	Sequence 76, Appl
27	73.6	6.9	958	15	US-10-128-714-1424	Sequence 1424, Ap
28	73.6	6.9	958	15	US-10-128-714-6424	Sequence 6424, Ap
29	73.6	6.9	2957	15	US-10-128-714-424	Sequence 424, App
30	73.6	6.9	2958	15	US-10-128-714-5424	Sequence 5424, Ap
31	71.4	6.6	988	9	US-09-323-998D-32	Sequence 32, Appl
32	70.2	6.5	954	9	US-09-323-998D-34	Sequence 34, Appl
33	70.2	6.5	960	9	US-09-323-998D-13	Sequence 13, Appl
34	70	6.5	846	16	US-10-320-797-2065	Sequence 2065, Ap
35	70	6.5	1639	17	US-10-389-566-224	Sequence 224, App
36	68.2	6.4	827	16	US-10-369-493-36552	Sequence 36552, A
37	67	6.2	1332	16	US-10-120-988-353	Sequence 353, App
38	67	6.2	1359	16	US-10-094-749-1226	Sequence 1226, Ap
39	67	6.2	1378	15	US-10-103-313-24	Sequence 24, Appl
40	67	6.2	1453	15	US-10-103-313-152	Sequence 152, App
41	62.8	5.8	409	10	US-09-918-995-17650	Sequence 17650, A
42	60.4	5.6	807	16	US-10-369-493-26033	Sequence 26033, A
43	60.4	5.6	807	16	US-10-369-493-26038	Sequence 26038, A
44	59.4	5.5	788	13	US-10-425-114-1629	Sequence 1629, Ap
c 45	59.4	5.5	820	13	US-10-425-114-16380	Sequence 16380, A

ALIGNMENTS

RESULT 1
US-09-323-998D-30